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Patent No. 5225337
Sequence 25, Appl
Sequence 30, Appl
                                                                                                         May 19, 2004, 02:49:51 ; Search time 74 Seconds (without alignments) 427.462 Million cell updates/sec
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Sequence 14,
Sequence 6,
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Sequence 12,
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Sequence 80,
Sequence 40,
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1: /cgn2 6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2 6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2 6/ptodata/2/ina/5A_COMB.seq:*

4: /cgn2 6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2 6/ptodata/2/ina/pcTuS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-739-158-40
US-08-739-158-40
US-08-739-167-40
US-08-40-796-40
US-08-931-869-40
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US-08-931-869-40
US-09-350-399-80
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29.2	9 15538	4	US-09-554-337-1	Sequence 1,	App
		4	US-09-814-951A-6	Sequence 6,	App
7.67	-	4	US-09-814-951A-1	Sequence 1,	App.
29.3		4	US-09-814-951A-3	Sequence 3,	App
28.8	5 85	Н	US-08-238-963A-12	Н	2, Ap
	11	4	US-09-579-182-1	Sequence 1,	App
28.4		m	US-08-602-791-1	Sequence 1,	App.
		٣	US-09-041-886-1	Sequence 1,	, Appli
		4	US-09-415-784-39	Sequence 35	9, Ap
28.2		4	US-09-415-785A-39	Seguence 35	9, Ap
28.2		4	US-08-944-465-39	e	9, Ap
4	5 56	4	US-09-415-868-39	m	9, Appl
28.2		4	US-09-415-900-39	c	
			ALIGNMENTS		

US-08-28-963A-18
Sequence 18, Application US/08238953A
Patent No. 5625047
GENERAL INFORMATION:
APPLICANT: Been, Michael D.
APPLICANT: Roseneterin, Sarah P.
APPLICANT: Perrotta, Anne T.
ITLE OF INVENTION: ENZYMATIC RNA MOLECULES
NUMBER OF SEQUENCES: 21
COURRESPONDENCE ADDRESS: 31
NUMBER OF SEQUENCES: 23
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite A700
CITY: Los Angeles
STREET: January 13, 1992
APPLICATION NUMBER: US/08/238,963A
FILING DATE: May 5, 1994
CLASSIFICATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION

Query Match 54.4%; Score 31; DB 1; Length 61;
Best Local Similarity 77.4%; Pred. No. 1.4;
Matches 41; Conservative 6; Mismatches 2; Indels 4; Gaps

US-08-238-963A-18

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CITY: Seattle
STATE: Washington
COUNTRY: US
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STATE: Washington
                                                                                                                                                                                                                                           ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Danez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polo, John M.
Ibanez, Carlos E.
Chang, Stephen M.W.
Jolly, Douglas J.
Belli, Barbara A.
Belli, EUKARROTIC LAYERED VECTOR INITIATION SYSTEMS
                                               UCCACCUCCUCGCGGUCCGACCUGGGCAU---CUUCGGAUGGCUAAGGGAGC 56
UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCGGCUUCGCAUGGCUAAGGGACC 56
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ZIP: 98104-7092

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,881
FILING DATE: 30-0CT-1996
CLASSITCATION: 435
ATTORNEY/AGRNT INFORMATION:
NAME: MCMMSsters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
TELECOMMUNICATION INFORMATION:
met FOLICH TO AND ADDITION:
TREECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          930049.423C6 / 1146.007
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32
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Patent No. 5789245
GENERAL INFORMATION:
APPLICANT: Dubensky Jr. Thomas W
APPLICANT: Dance, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Belli, Barbar A.
APPLICANT: Belli, Barbar A.
TITLE OF INVENTION: EUKARYOTIC LAYE
                                                                                                                                                                                                                                                                                           Sequence 40, Application US/08741881
Patent No. 5789245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILLEFANNE: (200) 622-357
TELEFAX: (200) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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Best Local Similarity
Matches 19; Conserve
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CORRESPONDED COLUMBIA Center, 701 Fifth Avenue
TITES: Seatcle
CITY: Seatcle
COMPUTER: PLODEY disk
COMPUTER:
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COMPUTER READABLE FORM:
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Sequence 80, Application US/08739158
Septent No. 5814482
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Dolly, Douglas J.
APPLICANT: Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
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                                                                                                                                                                                                                                                    Indels
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NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,158
FILING DATE: 30-OCT-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                        4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCG 35
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59.4%; Pred. No. 3.7;
tive 12; Mismatches
                                                                                                                                                                                                        Query Match 51'9%; Score 29.6; D
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 40, Application US/08739167
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INPORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single:
TYPE: TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELERAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Bet Local Similarity 59.**
....heg 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seattle
Washington
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US-08-739-167-40
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APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Danes, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Driver, David A.
APPLICANT: Briver, David A.
APPLICANT: Belli, Barbara A.
                                             APPLICANT: Jolly, Douglas J.
APPLICANT: DIJVEY, Douglas J.
APPLICANT: DIJVEY, DAVID A.
APPLICANT: DIJVEY, DAVID A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.9%; Score 29.6; DB 2; Length 52; 59.4%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/739,167
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AMETION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             930049.423C7 / 1146.008
                                                                                                                                                                                               B: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 80, Application US/08739167
Patent No. 5843723
GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 9300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEED and BERRY LLP
Ibanez, Carlos E.
Chang, Stephen M.
Jolly, Douglas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 59.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and 1
                                                                                                                                                                                                                                                                      Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seattle
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98104-7092
                                                                                                                                                                                                                                               CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                    g
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                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                        STREET:
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CORRESPONDENCE ADDRESS
ADDRESSEE: SEED and
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STATE: Washington
COUNTRY: US
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TOPOLOGY: linear
US-08-404-796-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 19; Conserv
          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
TOPOLOGY:
US-08-404-796-80
                                                                                                                                                                                                                                                                                                   US-08-404-796-80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
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Refeart No. 6015686

GENERAL INFORMATION:
APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Date S. Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Daiver, David A.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUGRRYOTIC LAYERED VECTOR INITIATION SYSTEMS NUMBER OF SEQUENCES: 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
GOMPUTER: IBM PC compatible
GOPFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,167
FILING DATE: 30-OCT-1996
CLASSIFCATION: 435
ATONEY/AGENT INFORMATION:
NAME: MCMASTERNIN DAVIG D.
RECISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
TELEPAX: (206) 682-6031
INFORMATION E: (206) 682-6031
INFORMATION REQUESTERISTICS:
LENGTH: 52 base pairs
TELEPAX: acid
TYPE: nucleic acid
TYPE: nucleic acid
TOPOLOGY: linear
US-08-739-167-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIPTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCMasters David D.
REGISTRATION NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPRAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 40;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     930049.423C7 / 1146.008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ELLING DATE: US/08/404,796
FILING DATE: 15-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 UCCACCUCCUCGCGGUNNNUGGGCAUGCG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.9%; Score 29.6; D
59.4%; Pred. No. 3.7;
tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-404-796-40
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                                                      Gaps
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                                                                                                                                                                                                                                                                                                                 APPLICANT: Dubensky Jr, Thomas W
APPLICANT: Polo, John M.
APPLICANT: Delo, John M.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Dily, Douglas J.
APPLICANT: Driver, David A.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NOMBER OF SEQUENCES: 128
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                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATER: PATEMIL Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,796
FILLING DATE: 15-MAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
    51.9%; Score 29.6; DB 3; 59.4%; Pred. No. 3.7; tive 12; Mismatches 1;
                                                                                                                             1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32
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                                                                                                  4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCG 35
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Sequence 40, Application US/08931869

Patent No. 6015694

GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dubensky Jr, Thomas W
                                                                                                                                                                                                                                                              ; Sequence 80, Application US/08404796 ; Patent No. 6015686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 80;
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
Query Match
Best Local Similarity 59.4<sup>†</sup>
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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STRANDEDNESS: single
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TYPE: nucleic acid
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TOPOLOGY:
US-08-931-869-80
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       APPLICANT: Ibanez, Carlos E.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Jolly, Douglas J.
APPLICANT: Jolly, Douglas J.
APPLICANT: Belli, Barbara A.
APPLICANT: Briver, Barli, Barbara A.
APPLICANT: Brown B. BURARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parent No. 6015694
GENERAL INFORMATION:
APPLICANT: Dubensky Jr. Thomas W
APPLICANT: Dubensky Jr. Thomas W
APPLICANT: Chang, Stephen M.W.
APPLICANT: Chang, Stephen M.W.
APPLICANT: Daily, Douglas J.
APPLICANT: Daily, Douglas J.
APPLICANT: Belli, Barbara A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 52;
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/931,869
FILING DATE: 16-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U$ 08/404,796
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: MCAMBABLERS
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 33,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                      E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.9%; Score 29.6; D
59.4%; Pred. No. 3.7;
ative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-931-869-80; Sequence 80, Application US/08931869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 59.4
Matches 19; Conservative
Polo, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                 CITY: Seattle
STATE: Washington
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seattle
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98104-7092
                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
TOPOLOGY:
US-08-931-869-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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Sequence 40, Application US/09350399

Patent No. 6342372
GENERAL INFORMATION:
GENERAL INFORMATION:
Dolo, John M.
Jolly, Douglas J.
Driver, David A.

TITLE OF INVENTION: EUGRARYOTIC LAVERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 51.9%; Score 29.6; DB 3; Length 52; Best Local Similarity 59.4%; Pred. No. 3.7; Matches 19; Conservative 12; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MCMABLERB, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,869
FILING DATE: 16-SEP-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/404,796
FILING DATE: 15-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: MCMSters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCG 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                         (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 61 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
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ACCOUNTRY.

JOHNSON TITLE OF INVENTION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

ADDRESSES:

CREESPONDENCES:

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

CREESPONDENCES:

CREESPONDENCES:

ADDRESSE:

CREESPONDENCES:

CREESPONDENCES:

COUNTRY:

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,140A
FILING DATE: 22-Jan-1999
CLASSIFICATION: «Unfanoun»
ATTORNEY/AGENT INPORMATION:
NAME: Cullman, Louis C.
RECISTRATION NUMBER: 39,645
RECISTRATION NUMBER: 39,645
TELEFRATION INPORMATION:
TELEFRANCE/DOCKET NUMBER: 20263.332 / 1146.020
TELEFRANCE (949) 823.6000
TELEFRANCE (949) 823.6000
                                                                                                                                                           TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
CITY: NEWPORT BEACH
STREE: CALIPORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۲,
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 40: US-09-236-140A-40
Ibanez, Carlos E.
Chang, Stephen M.W.
Jolly, Douglas J.
Driver, David A.
Belli, Barbara A.
                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 52 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 59.4
Matches 19; Conservative
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Polo, John M.
Jolly, Douglas J.
Driver, David A.
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                         Gaps
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52, Score 29.6; DB 4; Length 52;
Best Local Similarity 59.4%; Pred. No. 3.7;
Matches 19; Conservative 12; Mismatches 1; Indels
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ATTORNEY/AGENT IRFORMATION:
NAME: MCMGaters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/09/350,399
FILING DATE: 08-Jul-1999
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US-09-236-140A-40
; Sequence 40, Application US/09236140A
; Patent No. 6376236
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; Polo, John M.
                                        TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 80:
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Patent No. 6342372
GENERAL INFORMATION:
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      STRANDEDNESS: single
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TOPOLOGY: linear
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STATE: Washington
COUNTRY: US
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Best Local Similarity 59.4%
Matches 19; Conservative
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US-09-350-399-80
                                                                                                     US-09-350-399-40
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Gaps

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SOFTWARE: Patentin Release #1.0, Version #1.25

TURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/236,140A

FILING DATE: 22-3an-1999
CLASSIFICATION: «Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Culliman, Louis C.
REGISTRATION NUMBER: 39,645
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
TELEPHONE: (949) 823.600
TELEPHONE: (949) 823.600
TELEFAX: (949) 823.610

INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: uncleic acid
STRANDEDNESS: single
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-236-140A-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 51.9%; Score 29.6; DB 4; Length 52; Best Local Similarity 59.4%; Pred. No. 3.7; Matches 19; Conservative 12; Mismatches 1; Indels
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Search completed: May 19, 2004, 04:52:40 Job time : 88 secs

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30.2 53.0 382 10 AW681122 AW681122 WS1_8_E02 30.2 53.0 405 10 AW681043 AW681043 AW681043 WS1_8_E02 30.2 53.0 448 10 AW283452 AW283452 LG1_272_E 30.2 53.0 726 10 BF686394 BF686394 602143774	.2 53.0 807 10 BE902113 8 52.3 538 10 BE682984	.8 52.3 808 12 .8 52.3 808 12 .8 52.3 823 29 .4 51.6 495 12	.4 51.6 513 10 BE386169 .4 51.6 1057 12 BM553956 .2 51.2 123 9 AU077016 .2 51.2 222 14 CF122359	.2 51.2 257 12 BM798569 .2 51.2 300 9 AU09997 51.2 51.2 349 14 CB126416	.2 51.2 370 9 AL701336 .2 51.2 380 14 CB144469	.2 51.2 428 14 CF144607 2 51.2 453 12 BM836423	2 51.2 453 14 CELZEL144 2 51.2 481 14 CE113346	2 51.2 496 2 51.2 496 2 51.2 496 51.2 496	2 51.2 503 10 BE269642 2 51.2 507 14 CB140642	.2 51.2 508 10 BE296622 .2 51.2 511 12 BI053587	.2 51.2 513 14 CB141699 .2 51.2 513 28 AQ294266	.2 51.2 516 10 BE296669 .2 51.2 516 14 CB114356	.2 51.2 519 14 CB125200 .2 51.2 529 14 CB125108	.2 51.2 529 14 CB146530 .2 51.2 533 10 BR304959 51.2 51.4 CR176708	PILICIMENTIC			CF552723 AGENCOURT 1559533	IMAGE:30529107 57, MIXIN CF552723 CF552723.1 GI:34889557	EST.	Homo sapiens Rukarvota: Metazoa: Chordata:	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. E 1 (bases 1 to 857)	S NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) L. Unnublished (1999)	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics	National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892	Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Michael Brownstein	constitutions frequencies. Introduce Consortium (LLNL) constitution Library Arrayated by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
77 40 70		c 12 132 14						0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0						0 0 0 4 4 4 6 4 4 7			RESULT 1 CP552723/c	LOCUS	ACCESSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS TITLE JOURNAL	COMMENT			
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: May 19, 2004, 02:46:06; Search time 3211 Seconds (without alignments) 530.098 Million cell updates/sec	Title: RIBOZYMEIA Perfect score: 57 Sequence: 1 goguccaccucacgounuucgcauggcuaagggaccc 57	able: IDENTITY_NUCDX GARDOD 10.0 GARDEX 1.0	seqs; 1493	Total number of hits satisfying chosen parameters: 55026578	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	)— —	1:	3: em_estin:* 4: em_estmu:*	5: em_estov:* 6: em_estpl:*	7: em estro:* 8: em htc:*	9: gb_est1:*  10: gb_est2:* 11: ch_hrc:*	12: gb_get3:* 13: gb_est4:* 14: object4:*	15: em_estfun:* 16: em_estfun:*	17: em_gss_hum:* 18: em_gss_hum:*			24: em_gss_pro:* 25: em_gss_pro:*	em 988		No. is the number of results predicted by orester than or equal to the score of the			Result Query No. Score Match Length DB ID Description	C 1 32.2 56.5 857 14 CP552723 CP552723 AGENCOURT C 2 32 56.1 1182 12 B1457296 B1457296 603185617 3 31.4 55.1 622 29 CC526419 CC526419 CC526419 CH240 401 C 4 30.6 53.7 869 14 CB991305 CB991305 AGENCOURT

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CC526419.1 GI:31844707
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                       Query Match
Best Local Similarity 52.3%
Matches 23; Conservative
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Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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JOURNAL
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
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CC526419
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/mol_type="mRNA"
/db_xefe="texaon:9606"
/clone="INAGE:528380"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC_42"
/clone lib="NIH MGC_42"
/clone lib="NIH MGC_42"
/clone lib="NIH MGC_42"
/clone lib="Texaon: paracress; Vector: poTB7; Site_1: XhoI;
Site_2: ECRI; cDNA made by oligo-dT priming.
Directionally cloned into ECRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Size-selected -550bp
for average ineart size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MCC Library. |"
                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="Laxon:9806"
/db_xref="Laxon:9806"
/lab_host="MAGE:30529107"
/lab_host="Pinand Tolad"
/clone=lib="NIH_MGC 183"
/note="Organ: Pooled muscle (cardiac and skeletal);
/note="Organ: Pooled muscle (cardiac and skeletal);
/note="Organ: Pooled muscle (cardiac and skeletal);
/note:profile in Site_1: EcoRV (destroyed); Site_2:
/not1; Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.7. Library was constructed by Invitrogen."
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603185617F1 NIH_MGC_42 Homo gapieng cDNA clone IMAGE:5258380 5',
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov a column: 05
High quality sequence stop: 335.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1182)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGUCCACCUCCUCGCGGUNNNDNNUGGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
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                       Plate: NDAM616 row: c column: 04
                                            High quality sequence stop: 680.
Location/Qualifiers
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http://image.llnl.gov
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BI457296/c
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovinae; Bos.

Bovinae; Borinae; Bos.

1 (bases 1 to 622)

1 (bases 1 to 622)

1 Sai, Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Mathewson, C., Wye, N., Matra, M., de Jong, P., Keele, J.W. and Kappes, S.M. Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478 Unpublished (2003)

Contact: Rob Holt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rholt@bcggsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Seq primer: Spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
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                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Far: 604-877-6085
Fax: 604-877-6276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 CCTCCTCCTCGCGGTGTGGATGGGGCGTCCATCTCCCACCTGCCTCAGGCCCCC 156
                                                                                                                                                                                                                                                                                                                    CH240_401C15.TARBAC13P2 CHORI-240 BOB taurus genomic clone CH240_401C15, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 CCACCUCCUCGCGGUNNNDNNUGGGCAUGCGUUCGCAUGGCUAAGGGACCC 57
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/cell type="Blood"
/clone lib="CHORI-240"
/note="Vector: pTARBACI.3; Site_1: MboI; Site_2:
Hereford bull L1 Domino 99375; CHORI-240 Bovine
library (Male) produced by Pieter de Jong"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.1%; Score 31.4; DB 29; Length 622; 50.9%; Pred. No. 1.5e+03; ive 13; Mismatches 13; Indels 0
   Length 1182;
                                                                                                                                                               827 TCCTCGTCCTCGCGGTCGGTTGTGGGATTCGGCTTCGCTGGGC 784
56.1%; Score 32; DB 12; Length 11
52.3%; Pred. No. 1.3e+03;
ive 14; Mismatches 7; Indels
                                                                                                                           4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCGGCUUCGCAUGGC
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/strain="breed: Hereford"
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/clone="CH240_401C15"
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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

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/clone lib="water-gressed 1 (WS1)"
/rotome lib="Water-gressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda Zap; Site 1: Xho1; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
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                                                                                                                                                                                                                                                                                                       Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 405)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
                                                                          Unpublished (2000)
Contact: Cordonnier-Paratt MM
Contact: Cordonnier-Paratt MM
Contact: Cordonnier-Paratt MM
Liaboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Far: 706 542 1860
Pax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
  Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 GGTTCCAGCTCCTCCACGACCTGGCTGATCGCATTAGCATGGCAAGGGAC 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.0%; Score 30.2; DB 10; Length 382; 49.1%; Pred. No. 2.6e+03; ive 13; Mismatches 15; Indels 0.
                               Pratt, L.H.
An EST database from Sorghum: water-stressed plants
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Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
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                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 382
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High quality sequence stop: 405
POLYA=No.
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                                                                                                                                                                                                                                                                          Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW681043
AW681043.1 GI:7554749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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High quality s
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/foloe= lib= NIH MGC 148"
/incte= Organ: placenta; Vector: pBluescriptR; Site_1:
all -Xhol; Site_2: BamH; Library is oligo-dr primed_and
directionally cloned using primer
5'-TTTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert
size 2.3 kb and normalized to RT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIMH/NHGRI,
National, Institutes of Health). Note: this is a NIH_MGC
Library.
                                                                    CB991305
AGENCOURT 13666258 NIH MGC 148 Homo sapiens cDNA clone IMAGE:30332633 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW681122 382 bp mRNA linear EST 19-JUL-2000 WS1 8 E02.gl A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM349 row: p column: 18
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Sorghum bicolor
Sorghum bicolor
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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National Institutes of Health, Mammalian Gene Collection (WGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGB:3033263"
/issue_type="pre-eclamptic placenta"
/lab_hogt="DH10B TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.7%; Score 30.6; DB 14
51.0%; Pred. No. 2.8e+03;
ilve 13; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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Best Local Simi
Matches 25;
                    RESULT 4
CB991305/c
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DEFINITION

RESULT 5 AW681122

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BE902113
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/db_xref="taxon:4558"
/clone_lib="Light Grown (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site 1: XhoI; Site 2:
BCORI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were
/mol_type="mRNA"

/do xref="texon:4558"
/clone lib="Water-stressed 1 (WS1)"
/clone lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda Zap; Site 1: Xho1; Site 2: EcoR1; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
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LG1_272_E01.91_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
sequence.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
1 (bases 1 to 448)
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Sequences have been trimmed to exclude PolyA, vector and regions
Sequences have been trimmed to exclude PolyA, vector and regions
ablow Phred quality 16. The threshold for high quality sequence is
20. Three-prime sequences, which are obtained with PolyTWix or T7
sequencing primer, are presented as the reverse complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H. An SST database from Sorghum: light-grown seedlings Unpublished (2000)
On Jan 6, 2000 this sequence version replaced gi:6857936.
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                     Length 405;
                                                                                                                                                                                                                                                                15; Indels
                                                                                                                                                                                                                       DB 10;
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                                                                                                                                                                                                                     53.0%; Score 30.2; DB 10 ilarity 49.1%; Pred. No. 2.6e+03; Conservative 13; Mismatches 15
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/organism="Sorghum bicolor"
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High quality sequence stop: 448
POLYA=Yes.
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Fax: 706 583 0210
                                                                                                                                                                                                                                            Similarity
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AW283452
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EST 22-DEC-2000
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NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 726)
NIH-MGC http://mgc.noi.nih.gov/.
                                              602143774F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304611 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Induction institutes of negatin, mammairan Sens Collection (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbe-remail.nih.gov

Tisaus Proparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CON Action Hongle Hong Ling Action (A.G.E. Consortium/LLNL)

CON Action Ling Ling Consortium/LLNL at:

High quality sequence stop: 691.

High quality sequence stop: 691.

Location/Consortium/LLNL
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     linear
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_46"
     mRNA
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/db_xref="taxon:9606"
/clone="IMAGE:4304611"
     726 bp
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Matches 28; Conservative
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                                                                                                                                                                                                                                                                                           /mol type="mrRNA"
/db_xref="taxon:9606"
/clone="INMES.3957479"
/tissue_type="choriocarcinoma"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC_21"
/clone lib="NIH MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Single pass sequencing. Bases called and alt trimmed with phred
vo. 980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 25-APR-2001
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, B., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keele, J.W.
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                 cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Theorye Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCW835 row: d column: 24 High quality sequence stop: 778.
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PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366;
Fax: 402 762 4390
    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                      1. .807 |
/organism="Homo sapiens"
                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                 Location/Qualifiers
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FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
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Contact: Smith TPL
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602259070F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4342409 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabe-remail.nih.gov.
Tissue Procurement: Louis Staudt, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LlAM9957 row: k column: 18
High quality sequence stop: 716.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 777)
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/lab.host="Nmphona, cell line"
/lab.host="NHH MGC_08"
/clone_lib="NHH MGC_08"
/note="Gorgan: lymph; Vector: pCWV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size_1:867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NH_MGC Library."
                                                                                                                                                                                                       /tissue_type="pooled"
/lab host="DH108"
/clome_lib="WARC 4BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue From day 20 and day 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (Dases 1 to ''')
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 538;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 TGCACCTCCCTGAGCTTCCTGGTGGGCTTGCAGCTTCCCCTGGCT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCGCUUCGCAUGGCU 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.3%; Score 29.8; DB 10;
46.7%; Pred. No. 3.8e+03;
iive 15; Mismatches 9;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4342409"
                                                                                                                        organism="Bos taurus"
Plate: 84 row: O column: 20 Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9913"
                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF796052.1 GI:12101106
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Email: rholt@bogsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
Plate: 395 row: G column: 6 Seq primer: SP6 Class: BAC ends.
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Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A.,
Schein,C., Warra,M., Masson,A., Brown-John,M., Jones,S.,
Schein,J., Marra,M., Ge Jong,P., McWilliam,S., Barris,W.,
Dalrymple,B.P. and Tellam,R.
Bevine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Unpublished (2003)
Other GSSs: CH40-395G6.T7
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1 (bases 1 to 495)
Kohara, Y., Shin-1,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H. Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /coll type="Blood"
/clone lib="CHORL-240"
/note="Vector: PTARBACI.3; Site 1: Mbol; Site 2: Mbol;
Hereford bull Li Domino 99375; CHORL-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                          Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada VSZ 486
Far: 604-877-6085
Fax: 604-877-6276
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="breed: Hereford"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryzias latipes (Japanese medaka)
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/clone="CH240_395G6"
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BJ004361.1 GI:17355872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
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Best Local Similarity
Matches 21; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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BJ004361/c
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Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                               BM006402 808 bp mRNA linear EST 30-OCT-2001 603615114F1 NIH_MGC_110 Homo saplens CDNA clone IMAGE:5421075 5',
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1 (bases 1 to 823)
Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: ggapbs-rémail.nih.gov
Tisaue Procurement: ATCC
Tisaue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LLCMI876 row: 1 column: 04
High quality sequence stop: 552.
High quality sequence stop: 552.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 808)
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  268 TCCACCTCCTCCTGGCTGAGCACCGTCCTGGGGCCTTCCATGGCAGAGGGTCC 216
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CH240_395G6.TARBAC13P2 CHORI-240 Bos taurus genomic clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db Arzef="team.NA"
/clone="IMAGE:5421075"
/tiseue_type="ductal carcinoma, cell line"
/lab host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC_110"
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GSS.
Bos taurus (cow)
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Matches 27; Conserv
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CC593873
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PEATURES

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/tissue type="melanotic melanoma"
/lab.host='muluo (phage-resistant)"
/clone lib="NIH MGC 20"
/clone line BcoxI(XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 513)
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM279 row: f column: 04
High quality sequence start: 15
High quality sequence start: 15
High quality sequence stop: 513.
Location/Qualifiers
L. CALLON CALLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCGGCUUCGCAUGGCUAAGGGA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Indels
                                                                                                                                                                                                                                                                                                                                                                             /sex="mixture of female and male"
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1 Similarity 47.1%; Pred. No. 4.8e+03;
24; Conservative 14; Mismatches 13;
                                                                                                                                                                             organism="Oryzias latipes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/clone="MF01SSA064D03"
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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KEYWORDS
SOURCE
ORGANISM
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BE386169/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                           FEATURES
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1 GGGUCCACCUCCUCGCGGUNNNDNNUGGGCAUGCGGCUUCGCAUGGCUAAG 51
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Search completed: May 19, 2004, 04:51:37 Job time : 3251 secs

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Gaps

ö

51.6%; Score 29.4; DB 10; Length 513; 49.0%; Pred. No. 4.9e+03; tive 13; Mismatches 13; Indels 0;

Conservative

Best Local Similarity Matches 25; Conserv

Query Match

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CDNA COLT Nucleotid Plasmid p DNA HCV I SFV ECORV RNA HCV I Plasmid p Plasmid p Plasmid p Vesicular Vesicular Vesicular

Self-clea Self-clea Hepatitis EPO gene Hepatitis Clone del

Aaq53138 Aaq51140 Aaq46665 Aaq46665 Aaq46663 Aaq4663 Aaf84035 Aaf84035 Abz 82120 Abz 82120 Abz 82121 Abz 82121 Abz 82121 Abz 7701 Ab

AAQ53138 AAQ53140 AAQ46665 AAQ46665 AAAQ46666 AAF84035 AAF84035 AAF82121 AAN82174 AAN82174 AAAY3131 AAT78131 AAT78131 AAT78131 AAT78131 AAT78131 AAT78131 AAT78131

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44444 44444 44444 44444 44444 44444 44444 44444 44444

	Copyright (c	GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.		
OM nucleic - nuc	- nucleic search, u	using sw model	•	
Run on:	May 19, 2004, 01:34:20 ;	<pre>01:34:20 ; Search time 403 Seconds</pre>	es/sec	
Title: Perfect score: Sequence:	RIBOZYME1A 57 1 ggguccaccuc	RIBOZYMELA 57 1 ggguccaccuccucgcggunuucgcauggcuaagggaccc	57	
Scoring table:	IDENTITY NUCDX Gapop 10.0 , Gapext 1.0	apext 1.0		
Searched:	3373863 seqs,	3373863 segs, 2124099041 residues		
Total number of	hits satisfyin	Total number of hits satisfying chosen parameters: 6747726		
Minimum DB seg length: 0 Maximum DB seg length: 200000000	length: 0 length: 200000	000		
Post-processing: Minimum Match 0% Maximum Match 10 Listing first 45	Minimum Match Maximum Match Listing first	0% 100% 45 summaries		
Database :	N. Geneseq. 29Jan04:* 1: geneseqn1980s:* 2: geneseqn2000s:* 4: geneseqn2001as:* 5: geneseqn2011as:* 6: geneseqn201bs:* 7: geneseqn2001bs:* 8: geneseqn2003bs:* 9: geneseqn2003bs:* 10: geneseqn2003bs:*	an04:* 80s:* 90s:* 010s:* 01bs:* 03as:* 03cs:*		
Pred. No. score gree and is der	is the number ster than or eq rived by analys	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	a cinted,	
	de	SUMMARIES		
Result No. Score	Query Match Length DB	B ID Description	uc	

ALIGNMENTS

		Description	Aaz57636 Trans-act	Aaz57637 Trans-act	Aaz57638 Trans-act	Aaz57639 Nucleotid	Aaq46667 Substrate	e	Aaq86204 Sindbis/H	Aat31151 HDV rever	Aat30817 HDV riboz	Aav42394 Nested PC	Aav42426 Forward P	Aav60154 Nested PC	Aav60185 Reverse P	Aav70746 Reverse P	Aav70714 Nested pr	0	Aaz92970 Hepatitis	6	m	0	Aal38810 Alphaviru	Abk46276 HDV antig	Abk46316 Hepatitis
	SUMMARIES	ID	3 AAZ57636	3 AAZ57637	3 AAZ57638	3 AAZ57639	2 AAQ46667	2 AAQ86173	2 AAQ86204	2 AAT31151	2 AAT30817	2 AAV42394	2 AAV42426		2 AAV60185	2 AAV70746	2 AAV70714		3 AAZ92970	3 AAZ92843	3 AAZ92803	5 AAL38850	5 AAL38810	5 ABK46276	5 ABK46316
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		Length	! !																						
	de	Query Match	98.6	98.6		60.7	54.4	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	ä	;	51.9	ä	51.9
			56.2	56.2	46.6	34.6	31	6.	٥.	6.	29.6	6	6.	29.6	φ.	•	29.6	φ.	φ.	٩.	29.6	φ.	29.6	e,	29.6

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Trans-acting inherited dis inherited dis Synthetic. ' Key misc_binding stem_loop misc_binding stem_loop misc_binding stem_loop w09955856-A2. 04-NOV-1999. 29-APR-1999; 29-APR-1999; 29-APR-1999; WPI; 2000-096 New construct diagnostic an	<b>1</b>	05-APR-2000	(first entry)
Trans-acting antigenomic delta ribozyme; viral RNA cleavage; inherited disease; deltaRzPl.1; ss.  Synthetic.  Key  misc_binding 16  /*tag= a //note= "Forms double stranded region with bases 5:	· 图 :	Trans-acting	antigenomic delta ribozyme, deltaRzP1.1 nucleotide sequence
Synthetic.  Key  misc_binding 16  /*tag= a /*note= "Forms double stranded region with bases 5: 719  misc_binding 725  wisc_binding 2025  %*tag= b /*tag= c /bound moiety= "SP1.1 substrate (AAZ57641) bases 3: 3045  misc_binding 5257  /*tag= c //note= "Forms a double stranded region with bases W09955856-A2.  04-NOV-1999.  29-APR-1999; 99WO-CA000391.  29-APR-1999; 99GA-02230203.  (UYSH ) UNIV SHERBROOKE.  Perreault J, Ananvoranich S, Lafontaine D; WPI; 2000-096791/08.  New construction of nucleic acid enzyme useful for biotechnological diagnostic and therapeutic applications.	(25)	Trans-acting inherited dis	antigenomic delta ribozyme; viral RNA cleavage; ease; deltaRzPl.1; ss.
misc_binding 16  /*tag= a	SOS		
misc_binding 16  /*tag= a  stem_loop	4 E	Kev	Location/Onalifiers
#ttag= a /*ttag= a /*ttag= a /*ttag= a /*ttag= b /*ttag= b /*ttag= b /*ttag= b /*ttag= c /*ttag= e /*ttag=	E	misc_binding	1.6
stem_loop 719  misc_binding /*tag= b  stem_loop /*tag= c /*tag= c /*bound moiety= "SP1.1 substrate (AAZ57641) bases is tem_loop /*tag= d /*tag= e //note= "Forms a double stranded region with bases w09955856-A2.  04-NOV-1999. 29-APR-1999; 99WO-CA000391. 29-APR-1999; 99CA-02230203. (UYSH ) UNIV SHERBROOKE. Perreault J, Ananvoranich S, Lafontaine D; WPI; 2000-096791/08. New construction of nucleic acid enzyme useful for biotechnological diagnostic and therapeutic applications.	H		a "Forms double stranded region with bases
misc_binding /0.25 /*tag= c /*tag= c /*tag= c /*bound moiety= "SP1.1 substrate (AAZ57641) bases if bound moiety= "SP1.1 substrate (AAZ57641) bases if bound moiety= "SP1.1 substrate (AAZ57641) bases /*tag= d /*tag= d /*tag= e //note= "Forms a double stranded region with bases w09955856-A2.  04-NOV-1999.  29-APR-1999; 99WO-CA000391.  29-APR-1998; 98CA-02230203.  (UYSH ) UNIV SHERBROOKE.  Perreault J, Ananvoranich S, Lafontaine D;  WPI; 2000-096791/08.  New construction of nucleic acid enzyme useful for biotechnological diagnostic and therapeutic applications.	F F	stem_loop	
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stem_loop 3045  /*tag= d misc_binding 5257 /*tag= e /note= "Forms a double stranded region with bases W09955856-A2.  04-NOV-1999. 29-APR-1999; 99WO-CA000391. 29-APR-1998; 98CA-02230203.  (UYSH ) UNIV SHERBROOKE. Perreault J, Ananvoranich S, Lafontaine D; WPI; 2000-096791/08. New construction of nucleic acid enzyme useful for biotechnological diagnostic and therapeutic applications.	F F		c moietv= "SP1.1 substrate (AAZ57641) bases
misc_binding /*tag= d /*tag= e //note= "Forms a double stranded region with bases W09955856-A2. 04-NOV-1999. 29-APR-1999; 99KO-CA000391. 29-APR-1998; 98CA-02230203. (UVSH ) UNIV SHERBROOKE. Perreault J, Ananvoranich S, Lafontaine D; WPI; 2000-096791/08. New construction of nucleic acid enzyme useful for biotechnological diagnostic and therapeutic applications.	댎	stem_loop	
/*tag= e //note= "Forms a double stranded region with bases W09955856-A2. 04-NOV-1999. 29-APR-1999; 99WO-CA000391. 29-APR-1998; 98CA-02230203. (UYSH ) UNIV SHERBROOKE. Perreault J, Ananvoranich S, Lafontaine D; WPI; 2000-096791/08. New construction of nucleic acid enzyme useful for biotechnological diagnostic and therapeutic applications.	F F	misc binding	
/note= "Forms a double stranded region with bases W09955856-A2. 04-NOV-1999. 29-APR-1999; 99WO-CA000391. 29-APR-1998; 98CA-02230203. (UYSH ) UNIV SHERBROOKE. Perreault J, Ananvoranich S, Lafontaine D; WPI; 2000-096791/08. New construction of nucleic acid enzyme useful for biotechnological diagnostic and therapeutic applications.	H	ı	
	FX		"Forms a double stranded region with bases
	Z X	WO9955856-A2.	
	€ E ×	04-NOV-1999.	
	F X	29-APR-1999;	99WO-CA000391.
	E	29-APR-1998;	98CA-02230203.
	4 A X	UYSH ) UNIV	SHERBROOKE.
	됩	Perreault J,	Lafontaine
	<b>3</b> 83	WPI; 2000-096	791/08.
	ξ <u>Ε</u>	New construct	ion of nucleic acid enzyme useful for biotechnological,
	ΡŢ	diagnostic ar	d therapeutic applications.

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ribozymela.rng

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05-APR-2000
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                                                                                        Synthetic.
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                                                                                                               stem_loop
                                                                    AAZ57637
                                         Query Match
                                           Local
                                             Matches
                                                            RESULT 2
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cleaves substrate SPI.2 (see AAZ57634). The invention relates to a nucleic acid enzyme (e.g. delteRzPl.2) that is constructed to have a substrate binding portion with the following sequence 3'-UNKNN-5'. The substrate of the enzyme has the sequence 5'-H*GNNHN-3'. The binding portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the cleavage site of the substrate (cleavage site is represented by *). At least one nucleotide is present 5' to the cleavage site of the substrate nucleotide sequence at a specific cleavage site by mixing the substrate nucleotide sequence at a specific cleavage site by mixing the substrate with the enzyme. The enzyme is used to cleave a substrate with the enzyme. The enzyme diagnostic also have other therapeutic, biotechnological and diagnostic also have other therapeutic, biotechnological and diagnostic applications. Note: This sequence is not shown in the specification, but has been derived from the delteRzPl:1 sequence (AAZ57636) shown in figure 1
                                                                              nucleotide sequence of ribozyme deltaRzP1.2. This ribozyme strate SP1.2 (see AAZ57634). The invention relates to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
/bound_moiety= "SP1.1 substrate bases (AAZ57641) 5-11"
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30. .57
52. .57
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/note= "Forms a double stranded region with bases 6-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGUCCACCUCCUCGCGGUNNNDNNUGGGCAUGCGGCTUCGCAUGGCUAAGGGACCC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGUCCACCUCCUCGCGGUCCCAGCUGGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
inherited disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trans-acting antigenomic delta ribozyme nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.6%; Score 56.2; DB 3; 89.5%; Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perreault J, Ananvoranich S, Lafontaine D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
diagnostic and therapeutic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .6
/*tag= a
/note= "Forms d
                                        Example 1; Page; 52pp; English
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(first entry)
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05-APR-2000
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                                                   This is the nucleotide sequence of ribozyme deltaRzPl.1. This ribozyme cleaves substrate SPl.1 (see AAZS7641). The invention relates to a nucleic acid enzyme (e.g. deltaRzPl.1) that is constructed to have a substrate binding portion with the following sequence 3'-UNNXNN-5'. The substrate of the enzyme has the sequence 5'-H'*GNNHNN-3'. The binding portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the cleavage site of the substrate (cleavage site is represented by *!). At least one nucleotide is present 5' to the cleavage site of the substrate sequence. The enzyme of the invention is used to cleave a substrate nucleotide sequence at a specific cleavage site by mixing the substrate with the enzyme. The enzyme is used to cleave viral RNA or RNA causing for example an inherited disease. The enzymes also have other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prans-acting antigenomic delta ribozyme, deltaRzP1.2 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7. .19
/*tag= b
20. .20
/*tag= c
/bound_moiety= "SP1.2 gubstrate bases (AAZS7634) 6-11"
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/*tag= e
/note= "Forms a double stranded region with bases 6-1"
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*tag= a
note= "Forms double stranded region with bases 52-57"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGUCCACCUCCUCGCGGUNNNDNNUGGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New construction of nucleic acid enzyme useful for biotechnological,
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trans-acting antigenomic delta ribozyme; viral RNA cleavage;
inherited digease; deltaRzPl.2; ss.
                                                                                                                                                                                                                                                                                                                                                                                    Score 56.2; DB 3; Length 57;
Pred. No. 1.4e-07;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                    Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lafontaine D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                   Example 1; Fig 1A; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ananvoranich S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ57637 standard; RNA; 57 BP
                                                                                                                                                                                                                                                                                                                                                                                          98.64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-CA000391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98CA-02230203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ט
                                                                                                                                                                                                                                                                                                                                                                                                                                51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHERBROOKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-096791/08.
                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VINU ( H2YU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perreault J,
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Gaps

Length 57; 0; Indels Lafontaine D;

98CA-02230203.

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This is the nucleotide sequence bimolecular ribozyme RzA fragment. This ribozyme cleaves substrate SP1.1 (see AAZ57641). The invention relates to a nucleic acid enzyme (e.g. deltaRzPl.1) that is constructed to have a substrate binding portion with the following sequence 3'-UNNXNN-5'. The substrate of the enzyme has the sequence 5'-H'*GNNHNN-3'. The binding portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3' to the cleavage site of the substrate (cleavage site is represented by *). At least one nucleotide is present 5' to the cleavage site of the substrate sequence. The enzyme of the invention is used to cleave a substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide sequence at a specific cleavage site by mixing the substrate with the enzyme. The enzyme is used to cleave viral RNA or RNA causing the example an inherited disease. The enzymes also have other therapeutic, biotechnological and diagnostic applications
                                                                                                                                                                                                                                                                      New construction of nucleic acid enzyme useful for biotechnological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37 BP; 3 A; 16 C; 12 G; 0 T; 6 U; 0 Other;
                                                                                                                                                                                                                                                                                                             diagnostic and therapeutic applications
                                                                                                                                                                                                                                                                                                                                                                        Example 5; Fig 4; 52pp; English
                                                                                                                                                     Perreault J, Ananvoranich S,
                                                                                       (UYSH ) UNIV SHERBROOKE.
                                                                                                                                                                                                               WPI; 2000-096791/08.
                         29-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
ö
                                                                                                                                                                                                                                      This is the nucleotide sequence of a trans-acting antigenomic delta ribozyme of the invention. This ribozyme cleaves substrate SP1.1 (see AAZ57641). The invention relates to a nucleic acid enzyme (e.g. deltaZ2P1.1) that is constructed to have a substrate binding portion with sequence 5'-H'*GNWHNN-3'. The binding portion of the enzyme (ribozyme) base pairs to 6 nucleotides 3'-UNNXNN-5'. The substrate of the enzyme has the cleavage site is represented by *). At least one nucleotide is present 5' to the cleavage site of the substrate invention is used to cleave substrate nucleotide sequence. The enzyme of the invention is used to cleave a substrate nucleotide sequence at a specific cleavage site by mixing the substrate with the enzyme. The enzyme is used co cleave a substrate with the enzyme is used co cleave the rapepeutic, biotechnological and disease. The enzymes also have other therapeutic, biotechnological and disease. The applications. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGUCCACCUCCUCGCGGUNNNDNNUGGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                       New construction of nucleic acid enzyme useful for biotechnological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%; Score 46.6; DB 3; Length 57; 78.9%; Pred. No. 0.00016; ive 6; Mismatches 6; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 57 BP; 7 A; 21 C; 19 G; 0 T; 10 U; 0 Other;
                                                                                                                           diagnostic and therapeutic applications
                                                                                                                                                                                     Example 1; Fig 2; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 78.9
Matches 45; Conservative
                      WPI; 2000-096791/08.
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Substrate; self-cleaving sequence; HDV; hepatitis delta virus; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= f
/label= stem_III
/note= "forms duplex with region 11. .13"
24. .30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11. .13 /*tag= e //labol= stem_III //note= "forms duplex with region 21. 23 //labol= stem_III //labol= "forms duplex with region 21. .23 //labol= 11. .23 //lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "forms duplex with region 52.
                                             GGGUCCACCUCCUCGGGUCCGACCUGGGCAUGCGCC 37
1 GGGUCCACCUCCUCGCGGUNNNDNNUGGGCAUGCGGC 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7..10
/*tag= b
/label= stem_II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Substrate-cleaving sequence ADC3.
                                                                                                                                                                                                                                           BP,
                                                                                                                                                                                                                                        AAQ46667 standard; RNA; 61
                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ರ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
13-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    duplex; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
stem_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stem_loop
                                                                                                                                                                                                                                                                                                             AAQ46667;
                                                                                                                                                                         ហ
                                                                                                                                                                                                        AAQ46667
                                                                                                                                                                         RESULT
                                                                 셤
                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /bound_moiety= "RzB fragment of bimolecular ribozyme" /note= "Forms double-stranded region with bases 20-16 of sequence AAZ57640"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20. .25 | // tag= c // bound moiety= "Ribozyme substrate Pl.1" // hound moiety= "Rorms double-stranded region with bases 11-6 of sequence AAZ57641"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= d
/bound molety= "RzB fragment of bimolecular ribozyme"
/note= "Forms double-stranded region with bases 8-1 of
sequence AAZ57640"
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Gaps

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1; Indels

60.7%; Score 34.6; DB 3; Length 37;

Pred. No. 1; 6; Mismatches

81.18;

30; Conservative

Matches

Nucleotide sequence of bimolecular ribozyme RzA fragment. Bimolecular ribozyme; viral RNA cleavage; RzA fragment; inherited disease; 88.

05-APR-2000 (first entry)

BP.

AAZ57639 standard; RNA;

AAZ57639 ID AAZ RESULT 4

ઠે d AAZ57639;

location/Qualifiers

Key misc\_binding

Synthetic.

/\*tag=

99WO-CA000391.

29-APR-1999;

WO9955856-A2

04-NOV-1999,

.37

misc binding

7. .19 /\*tag=

misc\_binding

stem\_loop

Similarity

Driver DA,

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The sequences given in AAQ86167-81 are primers which were used in the generation of plasmid DNA which initiates Sindbis infection. The sequences were used in the construction of a eukaryotic layered vector initiation system (ELVIS) derived from Sindbis. ELVIS's comprise a 5' sequence capable of initiating transcription of an alphavirus, a nucleotide sequence encoding alphavirus non-structural proteins, a viral junction region which has been inactivated such that viral transcription of the subgenomic fragment is prevented, and an alphavirus RNA polymerase recognition sequence. Inactivation of the viral junction region prevents transcription of the subgenomic fragment making vectors such as this suitable for a wide variety of applications, eg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR; transcription initiation; non-structural protein; subgenomic fragment; RNA polymerase recognition sequence; ELVIS; gene therapy; amplify; primer; polymerase chain reaction; cystic fibrosis; ss.
                                                                                                                                                                                                                                                                                         New alpha virus vectors for gene therapy - of viral infection, cancer, auto:immune disease, etc., and as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.9%; Score 29.6; DB 2; Length 51; 59.4%; Pred. No. 43; ive 12; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sindbis/HDV ribozyme sequence reverse primer, HDV17-68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 51 BP; 9 A; 20 C; 14 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                Jolly DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCG 35
                                                                                                                                                                                                                Chang SM,
                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 68; 260pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  品
                                                                           94WO-US010469.
                                                                                                                93US-00122791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ86204 standard; DNA; 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Conservative
                                                                                                                                                                                                                Ibanez CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                           (VIAG-) VIAGENE INC.
                                                                                                                                                                                                                                                      WPI; 1995-131362/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                  Dubensky TW,
WO9507994-A2
                                                                                                                  15-SEP-1993;
18-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09507994-A2
                                                                           15-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
23-NOV-1995
                                      23-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ86204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ86204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>.</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The self-cleaving sequences from genomic and antigenomic HDV can be used to develop enzymatic RNA mols. with similar properties. ADC3 is a smaller version of ADC1 (AAQ53138), wherein stem IV is shortened. Such a smaller enzymatic RNA has simplified synthesis and the potential for higher specific activity due to a higher probability that a small RNA will fold into an enzymatically active structure. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid molecule having RNA substrate-cleaving enzymatic activity -
useful for cleaving specific target molecules in=vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotic layered vector initiation system; Sindbis; alphavirus; PCR; transcription initiation; non-structural protein; subgenomic fragment; RNA polymerase recognition sequence; ELVIS; gene therapy; amplify; primer; polymerase chain reaction; cystic fibrosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer HDV17-68 amplifies vector DNA to initiate Sindbis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 UCCACCUCCUCGCGGUNNNDNNUGGCCAUGCGGCUUCGCAUGGCUAAGGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UCCACCUCGCGGGGCCGACCUGGGCAU---CUUCGGAUGGCUAAGGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 54.4%; Score 31; DB 2; Length 61; Best Local Similarity 77.4%; Pred. No. 16; Matches 41; Conservative 6; Mismatches 2; Indels
                                                *trag= i
label= stem IV
/note= "forms duplex with region 42. .45"
/*tag= g
/note= "RNA substrate binding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 61 BP; 10 A; 20 C; 19 G; 0 T; 12 U; 0 Other;
                                                                                                                                                  /2. .45
/*teg= j
/label= stem_IV
/note= "forms duplex with region 33.
52. .55
                                                                                                                                                                                                                                                                         /label= stem II
/note= "forms duplex with region 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perrota AT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 8, 55pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                93WO-US000292
                                                                                                                                                                                                                                                                                                                                                                                                                                                    92US-00821155
                                                                                                            34. .45
/*tag= h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ86173 standard; DNA; 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosenstein SP,
                                  33. .37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-243233/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYDU-) UNIV DUKE
                                        misc_structure
                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                12-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JAN-1992;
                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                    WO9314218-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
21-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                         22-JUL-1993
                                                                                                                  stem_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ86173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Been MD,
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Gaps

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93US-00122791. 94US-00198450.

15-SEP-1993; 18-FEB-1994;

Synthetic

RESULT 6

g

(VIAG-) VIAGENE INC

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Page

- of viral infection, cancer,

Polo JM;

Driver DA,

Jolly DJ,

Ibanez CE, Chang SM,

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The sequences given in AAQ86200-15 are primers which were used in the production of alphavirus vectors expressing multiple heterologous genes. These vectors are eukaryotic layered vector initiation systems (ELVIS) derived from Sindbis. ELVIS's comprise a 5' sequence capable of initiating transcription of an alphavirus, a nucleotide sequence encoding alphavirus non-structural proteins, a viral junction region which has been inactivated such that viral transcription of the subgenomic fragment is prevented, and an alphavirus RNA polymerase recognition sequence. Inactivation of the viral junction region prevents transcription of the subgenomic fragment making vectors such as this suitable for a wide variety of applications, eg. gene therapy for the treatment of cystic fibrosis. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alphavirus, Sindbis virus, vector, gene therapy, vaccine, polymerase chain reaction, PCR; primer, hepatitis delta virus, HDV,
                                                                                                                                                                                                                                                                                                                                     Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                            4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
51.34; cccc. ..
Best Local Similarity 59.44; Pred. No. 43;
Matches 19; Conservative 12; Mismatches
                                                                      New alpha virus vectors for gene therapy -
auto:immune disease, etc., and as vaccines
                                                                                                                 Example 7; Page 114; 260pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT31151 standard; DNA; 52 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HDV reverse primer HDV17-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-SEP-1996 (first entry)
                                          WPI; 1995-131362/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JAN-1995;
15-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribozyme; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9617072-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 9661-NUL-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT31151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
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Gaps

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1; Indels

DB 2; Length 52;

ö for the PCR amplification of HDV sequences. A second primer pair, SIN-HDV (AAT31152) and SIN276-SPE (AAT31153), is used to amplify a fragment contg. Sindbis 5'-end sequences fused to HDV sequences. Overlapping synthesis is used in a second round of PCR using primers HDV49-XC and SIN276-SPE. The resulting construct contains the expression cassette elements HDV ribozyme/Sindbis 5'-end 299 nts/Sindbis junction region/sindbis structural protein genes/Sindbis 3'-end untranslated region, designated pd5'26s. This was inserted into pcDNA3. Packaging cell line cassettes were constructed that allow inducible expression of structural proteins via alphavirus vectors Primer SHDVIF (AAT30816) contains a buffer sequence allowing enzyme digestion, a SacI site, and a hepatitis delta virus (HDV) ribozyme sequence. It was used with nested primer HDV17-68 (AAT30817) and reverse primer SHDV84R (AAT30818) to generate an HDV ribozyme. This antigenomic ribozyme can be placed between the polyA tract at the 3' end of a Sindbis virus-based eukaryotic layered vector initiation system, ELVIS, and the transcription terminal signals to produce alphavirus expression vectors useful in methods of gene therapy and for vaccine produ nucleotides 839-887. It was used with reverse primer HDV49-XC (AAT30850) New recombinant alpha-virus vectors - used to develop prods and methods for use in gene therapy and in the prodn. of vaccines. Gaps Driver DA; Alphavirus, Sindbis virus, vector, gene therapy, vaccine, primer, polymerase chain reaction, PCR, ELVIS, ribozyme, HDV, hepatitis delta virus, ss. ö DB 2; Length 52; Jolly DJ, 1; Indels Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other; Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other; Chang SMW, 1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32 4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCG 35 51.9%; Score 29.6; I 59.4%; Pred. No. 43; :ive 12; Mismatches Example 3; Page 85; 256pp; English. Ibanez CE, BP 94US-00348472. 95US-00376184. 95US-00405827. 95WO-US015490. HDV ribozyme primer HDV17-68. AAT30817 standard; DNA; 52 (CHIR ) CHIRON VIAGENE INC (first entry) Local Similarity 59.4 Polo JM, WPI; 1996-277785/28. Dubensky TW, WO9617072-A2 12-SEP-1996 30-NOV-1995; 30-NOV-1994; .8-JAN-1995; L5-MAR-1995; 36-JUN-1996 Synthetic. AAT30817; selli BĀ; Query Match Matches RESULT 9 AAT30817 88888888888888 g 

51.9%; Score 29.6; DB 2; Length 52;

Query Match

New recombinant alpha-virus vectors - used to develop prods and methods for use in gene therapy and in the prodn. of vaccines.

Primer HDV17-68 (AAT31151) is based on hepatitis delta virus (HDV)

Example 7; Page 120; 256pp; English

Driver DA

Jolly DJ,

Chang SMW,

Polo JM, Ibanez CE,

Dubensky TW, Belli BA;

WPI; 1996-277785/28.

(CHIR ) CHIRON VIAGENE INC.

94US-00346472. 95US-00376184. 95US-00405827.

95WO-US015490.

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PCR primers AAV42367-420 and AAV42422-54 are used in the course of the invention. The specification describes a DNA alphavirus structural protein expression cassette which comprises an inducible promoter and an alphavirus structural protein gene, where the promoter directs the expression of the alphavirus structural protein gene upon induction of the promoter within a cell, and where prior to induction within the cell, the expression cassette does not express sufficient quantities of structural proteins to be cytocoxic to a BHK cell containing the expression cassette. The products may be used to inhibit pathogens and
                                                                                                                         DNA alphavirus; structural protein expression; inhibit; pathogen; nmmune response; stimulate; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.9%; Score 29.6; DB 2; Length 52; 59.4%; Pred. No. 43; ive 12; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA alpha:virus structural protein expression cassettes recombinant alpha:virus particles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jolly DJ, Dubensky TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 7; Col 103; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                             93US-00122791.
94US-00198450.
94US-00348472.
95US-00376184.
95US-00404796.
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                                                                                                                                                                                                                                                                                                                                      96US-00741881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stimulate an immune response
                                                                              Forward PCR primer HDV17-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nested PCR primer HDV17-68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV60154 standard; DNA; 52
                             02-OCT-1998 (first entry)
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 59.4'
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chang SMW, Ibanez CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-446089/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1994;
30-NOV-1994;
                                                                                                                                                                                                                                                                                                                                      30-OCT-1996;
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04-DEC-1998
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                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV60154;
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         임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA alpha:virus structural protein expression cassettes - for producing recombinant alpha:virus particles.
                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA alphavirus; structural protein expression; inhibit; pathogen;
Immune response; stimulate; PCR primer; ss.
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                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCG 35
                                                                                                      1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32
                                                                                                                                                                                                                                                                                                                                                                                       Nested PCR primer HDV17-68 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Mismatches
59.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.9%; Score 29.6; 59.4%; Pred. No. 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Col 69; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jolly DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-00122791.
94US-00198450.
94US-00348472.
95US-00376184.
95US-00404796.
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                                                                                                                                                                                                                                               AAV42394 standard; DNA; 52 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-00741881
                             19, Conservative
                                                                                                                                                                                                                                                                                                                                         02-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chang SMW, Ibanez CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-446089/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 19; Conser
         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-1994;
30-NOV-1994;
20-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5789245-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                           AAV42394;
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Matches
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AAV42426
ID AAV42
XX
AC AAV42
                               Matches
                                                                                                                                                                                           RESULT 10
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LU AAV4

AAC AAV4

AAC AAV4

MAC AAV
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- for producing

Polo JM;

Driver DA,

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Eukaryotic layered vector initiation system; stimulate; immune response; sindbis; PCR primer; ss.
         1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32
4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCG 35
                                                                                                                                                                     Synthetic.
Hepatitis D virus
                                                                                                                                                                                                 US5814482-A
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AAV42426

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Gaps

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DUBE/)

XXCXX BARREY A PRINT BARREY BA

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Bukaryotic layered vector initiation system - containing eukaryotic promoter and heterologous antigen coding sequence, useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       precidentian describes an eugary of the process of the comprises a cukaryotic layered vector initiation system comprises a cukaryotic layered vector initiation system comprises a cukaryotic promoter 5' of viral cDNA which initiates, in a susceptible target cell, 5' to 3' synthesis of RNA from the viral cDNA. The RNA comprises a vector construct which autonomously amplifies in the cell and expresses a heterologous nucleic acid sequence which encodes an antigen or modified form that simulates an immune response to an animal. The system is useful for stimulating an immune response to an antigen by introducing the vector into target cells, preferably by infection in vivo, especially where the immune response is a cell mediated, HLA class I restricted or an HLA class II restricted immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              response. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primers AAV60184-85 are used in the course of the invention. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reverse PCR primer HDV17-68 used to amplify Hepatitis delta virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.9%; Score 29.6; DB 2; Length 52; 59.4%; Pred. No. 43; ive 12; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alphavirus vector construct; gene therapy; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                    Dubensky TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCG 35
                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Col 108; 144pp; English
                                                                                                                                                                                                                                                                    Jolly DJ,
                                   93US-00122791.
94US-00198450.
94WO-US010469.
                                                                                        94US-00348472.
95US-00376184.
95US-00404796.
96US-00739158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 59.4'
Matches 19; Conservative
                                                                                                                                                                       POLO J M.
DUBENSKY T W.
                                                                                                                                                                                                                                                                    Driver DA, Polo JM,
                                                                                                                                                                                                                                                                                                     WPI; 1998-541753/46
                                                                                                                                                                                                           JOLLY D J.
DRIVER D A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
Hepatitis D virus.
                                                                                                                                                                                                                                                                                                                                                                                  immune response.
 30-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAR-2003
02-FEB-1999
                                                           18-FEB-1994;
14-SEP-1994;
                                                                                          30-NOV-1994;
                                                                                                                                  LS-MAR-1995;
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                                                                                                                                                                   (POLO/)
                                                                                                                                                                                                           (JOLL/)
(DRIV/)
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                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotic layered vector initiation system - containing eukaryotic promoter and heterologous antigen coding sequence, useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribozyme sequence. The product is used in the course of the invention. The specifiaction describes an eukaryotic layered vector initiation system, based on Sindbis. The eukaryotic layered vector initiation system comprises a eukaryotic promoter 5' of viral cDNA which initiates, in a susceptible target call, 5' to 3' synthesis of RNA from the viral cDNA. The RNA comprises a vector construct which autonomously amplifies in the call and expresses a heterologous nucleic acid sequence which encodes an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              layered vector initiation system; stimulate; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen or modified form that stimulates an immune response within an animal. The system is useful for stimulating an immune response to an antigen by introducing the vector into target cells, preferably by infection in vivo, especially where the immune response is a cell mediated, HIA class I-restricted or an HIA class II-restricted immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primers AAV60153-55 are used to amplify Hepatitis delta virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   response. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                           Dubensky TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.9%; Score 29.6; D 59.4%; Pred. No. 43; ative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Col 71-72; 144pp; English.
                                                                                                                                                                                                                                                                                                                           Jolly DJ,
                                                                                                            94US-00198450.
94WO-US010469.
94US-00348472.
95US-00376184.
95US-00404796.
                                                       96US-00739158
                                                                                            93US-00122791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sindbis; PCR primer; ss
                                                                                                                                                                                                                                              DUBENSKY T W.
JOLLY D J.
DRIVER D A.
                                                                                                                                                                                                                                                                                                                         Driver DA, Polo JM,
                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-541753/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 19; Conserv
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Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                         immune response
                                                       30-OCT-1996;
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04-DEC-1998
                                                                                                                                                                                       15-MAR-1995,
                   29-SEP-1998
                                                                                            15-SEP-1993
                                                                                                                                  14-SEP-1994
                                                                                                                                                     10-NOV-1994
                                                                                                                                                                       18-JAN-1995
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(DRIV/)
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Gaps

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96US-00739167.

30-OCT-1996;

US5814482-A 29-SEP-1998

RESULT 13

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93US-00122791.

15-SEP-1993; 18-FEB-1994;

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                                                                                                                                                                                                PCR primers AAV70745-46 are used to amplify part of the hepatitis delta virus (HDV) genome. The amplified product is used in the production of the alphavirus vector constructs of the invention. These constructs comprise a promoter 5' of viral cDNA which initiates the synthesis of RNA from the viral cDNA by in vitro transcription, followed by a 5' sequence sequence encoding alphavirus nonstructural proteins, a viral junction region which has been inactivated such that viral transcription of a subgenomic fragment is prevented, an internal ribosome entry site or a subgenomic fragment is prevented, an internal ribosome entry site or a sequence which promotes ribosome read through between adjacent reading frames, and an alphavirus RNA polymerase recognition sequence. The recombinant alphavirus vectors can be used for gene therapy. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                       Alphavirus vectors constructs containing a 5' promoter of viral cDNA by in vitro transcription - used in gene therapy.
                                                                          Driver DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Driver DA;
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 52;
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                                                                          Ibanez CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alphavirus vector construct; gene therapy; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                             Sequence 52 BP; 9 A; 21 C; 14 G; 8 T; 0 U; 0 Other;
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                                                                          Chang SMW, Jolly DJ, Dubensky TW, Belli BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCG 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32
                                                                                                                                                                                                                                                                                                                                                                                                    51.9%; Score 29.6; D 59.4%; Pred. No. 43; ative 12; Mismatches
                                                                                                                                                                            Example 7; Col 103; 140pp; English
94US-00348472.
95US-00376184.
95US-00404796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-00198450.
94US-00348472.
95US-00376184.
95US-00404796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV70714 standard; DNA; 52 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 59.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang SMW, Jolly DJ,
Polo JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                                                                                                              WPI; 1999-044581/04.
                                                  (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
Hepatitis D virus.
30-NOV-1994;
20-JAN-1995;
15-MAR-1995;
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20-JAN-1995;
15-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAR-2003
02-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5843723-A.
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                                                                                       Polo JM;
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These conductors comprise a promoter 5 of viral cDNA which initiates the synthesis of RNA from the viral cDNA by in vitro transcription, followed by a 5' sequence which initiates transcription of alphavirus RNA, followed by a nucleotide sequence encoding alphavirus nonstructural proteins, a viral junction region which has been inactivated such that viral transcription of a subgenomic fragment is prevented, an internal viral cosme entry site or a sequence which promotes ribosome read through between adjacent reading frames, and an alphavirus RNA polymerase recognition sequence. The recombinant alphavirus vectors can be used for gene therapy. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                 Alphavirus vectors constructs containing a 5' promoter of viral cDNA by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.9%; Score 29.6; DB 2; Length 52; 59.4%; Pred. No. 43;
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                                                                                                                            in vitro transcription - used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TCCACCTCCTCGCGGTCCGACCTGGGCATCCG 32
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                                                                                                                                                                                                     Example 3; Col 69; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 59.4
Matches 19; Conservative
WPI; 1999-044581/04.
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DEFINITION
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
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AX012282
                                                 Result
                                                                      May 19, 2004, 01:36:25; Search time 3047 Seconds (without alignments) 810.815 Million cell updates/sec
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                                                                                                                                                     1 ggguccaccuccucgeggun.....uucgcauggcuaagggaccc
                                                                                                                                                                                                                                             6940544
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                   3470272 seqs, 21671516995 residues
                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                 using sw model
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Gapop 10.0 , Gapext 1.0
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em_htg_inv:*
em_htg_other:*
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em_htg_rod:*
em_htg_mam:*
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em_sy:*
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57
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Perfect score:
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PAT 06-SEP-2000 Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
Nucleic acid enzyme for rna cleavage
Patent: WO 9955856-A 44 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN A41844 Sequence 25 A41849 Sequence 30 105156 Sequence 11 D90192 Heparitis D D90190 Heparitis D D90190 Heparitis D 141385 Sequence 13 141386 Sequence 14 141378 Sequence 6 AR243300 Sequence AR342596 Sequence AR342597 Sequence Sequence Human DNA Mus muscu Mus muscu 141388 Sequence 16 AR123021 Sequence AX174839 Sequence BD226817 Alphaviru AR363756 Sequence Sequence Sequence Sequence 18 Sequence Sequence Sequence Sequence Homo sapi Homo sap AR183836 Sequence AR368179 Sequence AR368219 Sequence Sequence Sequence Sequence AX174838 Sequence X012282 Sequence Sequence Sequence Sequence Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. AR162377 AX012284 AX012291 AR062337 AC008429 linear RNA ALIGNMENTS AX012282 57 bp Sequence 44 from Patent W09955856. SUMMARIES HSA287B20 I41390 AR183836 AR368179 AR368219 AX174838 AX174839 BD226817 AR363756 AX012284 AR123021 HPDJS1 HPDJS2 HPDJM1 HPDJM2 AX012282 AX012282.1 GI:9998343 synthetic construct synthetic construct artificial sequences. 8 63.5 54.4 52.3 52.3 52.3 52.3 159423 52.3 17914 52.3 17914 52.3 17914 52.3 17914 52.3 17914 52.3 17914 52.3 Query Match Length

FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid enzyme for rna cleavage
Patent: WO 9955856-A 49 04-NOV-1999;
ANANVORANTCH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBEOCKE (CA)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ananvoranich, S., Lafontaine, D. and Perreault, J.P.

Nucleic acid enzyme for rna cleavage
Patent: W0 9955856-A 50 04-NOV-1999;

ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)

Location/Qualifiers
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                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                1 GGGTCCACCTCCTCGCGGTCCGGCCTGGGCATGCGGCTTCGCATGGCTAAGGGACCC
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                                     Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 98.6%; Score 56.2; DB 6; Length 5 I Similarity 71.9%; Pred. No. 1.3e-05; 41; Conservative 16; Mismatches 0; Indels
                                                                                                                                                                                                                                        linear
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                                                                         Indels
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                                   98.6%; Score 56.2; DB 6;
llarity 71.9%; Pred. No. 1.3e-05;
Conservative 16; Mismatches 0;
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xrefe"taxon:32630"
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/b xref="taxon:3260"
/noFe="synthetic nucleic acid"
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AX012288
AX012288.1 GI:9998349
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Sequence 49 from Patent WO9955856.
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Best Local Similarity 71.99,
The 41, Conservative
                                 Query Match
Best Local Similarity
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Best Local S:
Matches 41
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
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AX012288
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SOURCE
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Nucleic acid enzyme for rna cleavage
Patent: WO 9955856-A 48 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ananvoranich, S., Lafontaine, D. and Perreault, J.P.

Nucleic acid enzyme for rna cleavage
Batent: W0 995586-A 45 04-NOV-1999;

ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHEREROOKE (CA)

Location/Qualifiers
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                                                                                                                                                              1 98.6%; Score 56.2; DB 6; Similarity 71.9%; Pred. No. 1.3e-05; 11; Conservative 16; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
/mol_type="unassigned RNA"
/mol_txref="txxon:32630"
/nofe="synthetic nucleic acid"
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
                                 1..57
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:25630"
/note="synthetic nucleic acid"
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AX012286
                                                                                                                                                                                                                                                                                                                                                                 AX012283 57 bp
Sequence 45 from Patent W09955856.
 (CA); UNIV SHERBROOKE (CA)
                  Location/Qualifiers
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Best Local Similarity
Matches 41; Conserv
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PIERRE
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AX012286
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PAT 06-SEP-2000
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Nucleic acid enzyme for rna cleavage
Patent: WO 995585-A 46 04-NOV-1999;

PARANVORANICH SIRINARY (A) LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)

Location/Qualifiers
                                                                                                                                                                                     (CA); PERREAULT JEAN
                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGUCCACCUCCUCGCGGUNNNDNNUGGGCAUGCGGCUUCGCAUGGCUAAGGGACCC 57
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                                                                                                                                   Ananvoranich, S., Lafontaine, D. and Perreault, J.P. Nucleic acid enzyme for rna cleavage
Patent: WO 99558856-A 47 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA PIERRE (CA); UNIV SHERROOKE (CA)
Location/Qualifiers
                                                                                                                                                                                                                                  1.57
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="texon:32630"
/note="synthetic nucleic acid"
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/organism="synthetic_construct"
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81.8*; Score 46.6; DB 6
Best Local Similarity 64.9*; Pred. No. 0.012;
Matches 37; Conservative 14; Mismatches
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/db_xref="taxon:32630"
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Sequence 53 from Patent WO9955856.
AX012291.1 GI:9998352
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 Sequence 47 from Patent W09955856
                                   AX012285.1 GI:9998346
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artificial sequences
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AX012284
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Nucleic acid enzyme for rna cleavage
Parent: W0 995886-A 51 04-NOV-1999;
ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHEREROOKE (CA)

Location/Qualifiers
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PIERRE (CA); UNIV SHERBROOKE (CA)
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1 GGGTCCACCTCCTCGCGGTCCGAGCTGGGCATGCGGCTTCGCATGGCTAAGAGAACC
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Patent: WO 9955856-A 52 04-NOV-1999;
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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                                                                                                    AX012289 57 bp Sequence 51 from Patent W09955856.
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Sequence 52 from Patent WO9955856.
AX012290
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Best Local S:
Matches 41
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                                                                 RESULT 6
AX012289
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Direct Submission

Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. Email enquiries: humquery@sanger.ac.uk CB10 18A, UK. Email enquiries: humquery@sanger.ac.uk CB10 18A, UK. Email enquiries: humquery@sanger.ac.uk Clone requeets: clonerequest@sanger.ac.uk

On Jan 27, 2001 this sequence version replaced gi:8218066.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EmBL; Sw:, SWISSEROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP databases can be found at http://www.sanger.ac.uk/Projects/C leggans/wormpep This sequence chromosome 20, constructed by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/HGP/CHP200
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168545 bp DNA linear PRI 11-MAR-2001

Human DNA sequence from clone RP11-287B20 on chromosome 20 Contains
part of gene KIAA1272 for a protein similar to rat Tulip 2, ESTs,
STSs and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPII-287B20 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                               Nucleic acid enzyme for rna cleavage
Barent: Wo 995886-A 53 04-NOV-1999;
RABAVORANTCH SIRINART (CA); PERREAULT JEAN
PIERRE (CA); UNIV SHERBROOKE (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VECTOR, parcell of the control of clone IMPORTANT: This sequence is not the entire insert of clone IMPORTANT: This sequence is not the entire insert of clone RPI1-287B20 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RPI1-287B20 is at 1 in this sequence. The true right end of clone RPI-470C13 is at 111612 in this sequence. The true right end of clone RPI1-470C13 is at 111612 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 168545)
Griffiths, C.
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                                   Ananvoranich, S., Lafontaine, D. and Perreault, J.P.
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                                                                                                                                                                                                                                                                        /organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.5%; Score 36.2;
67.6%; Pred. No. 21
                                                                                                                                                                                                        Location/Qualifiers
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102652. 102807,104712. 104835,10555. 110626,
111814. 112586,120218. 120401,123707. 123844,
124131. 124199,125553. 125663,130988. 131096,
135464. 135104,135957. 136085,146005. >146133))
/gene="ba287B20.1" (ALO78634)
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/codon_start=1
/codon_start=1
/codon_start=1
/protein=1 and 2, isoform 1)"
/protein 1 and 2, isoform 1)"
/protein id="CAC27349.1"
/db_xref="SPTRMBL:098076"
/db_xref="SPTRMBL:098076"
/translation="DILNTIRHCPPRFFSLGFPGFSMLVGDPITAAARVLSTDILTA
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regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
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Em:AF041107 Em:AL050050 Em:AB033098
match: ESTE Em:T90823 Em:BE033098
Em:R05337 Em:T95728 Em:AW753998 Em:AW604552 Em:AW658646
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/note="LiMBB repeat: matches 5689. .6167 of consensus"
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/note="12 repeat: matches 2101. .2670 of consensus"
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/note="MER5B repeat: matches 1. .178 of consensus"
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/note="AluJb repeat: matches 1. .275 of consensus"
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/note="match: GSS: Em:AQ525450"

complement (9548..10038)

/note="match: GSS: Em:AQ772919"

10005..10404

/note="match: GSS: Em:AQ409384"

/gene="bA287520.1"
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/note="match: STS: Em:G57973
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/note="match: STS: Em:G55717
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                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                             /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="20"
/clone="RP11-287B20"
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                                                                                                                               Location/Qualifiers
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43783. .43862
/note="LIME3A repeat: matches 6030. .6117 of consensus"
43944. .44059
/note="LIME repeat: matches 5469. .5587 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Charlie4a repeat: matches 30. .501 of consensus" 3519. .38813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="LiMA7 repeat: matches 6075. .6273 of consensus"
2304. .32730
note="match: GSS: Em:AQ176627"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="AluSp repeat: matches 1. .312 of consensus" 1001. .21605 note="LIMB7 repeat: matches 5577. .6169 of consensus" 1618. .21818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2065. .22161
noce="12 repeat: matches 2577. .2716 of consensus"
3992. .2403. .2910
note="LIPA4 repeat: matches 6032. .6142 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                             note="LiM4 repeat: matches 5031. .5329 of consensus" 7900. .18040 consensus 5788. .5932 of consensus" note="LiM2 repeat: matches 5788. .5932 of consensus" 8042. .1832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="LiMB7 repeat: matches 5188. .5577 of consensus'
0690. .21000
                                                                                                                                                                                                                                         .6054. .16481

.note="match: GSS: Em:B47002"

.note="M.TIC repeat: matches 299. .466 of consensus"

.6740. .16951

.note="M.TIC repeat: matches 17. .237 of consensus"
                                                                              note="FLAM A repeat: matches 20. .135 of consensus" 5330. .15369 incte="MIR repeat: matches 106. .148 of consensus" 1535. .15474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="L2 repeat: matches 1921. .2661 of consensus"
1353. .37774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L2 repeat: matches 2515. .2748 of consensus"
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1378. 41532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="AluJo repeat: matches 1. .292 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat: matches 102. .208 of consensus"
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Note="WER5B repeat: matches 1. .175 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="AluJo repeat: matches 1. .298 of consensus" 3137. .19367
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                                                                                                                                                                        note="MIR repeat: matches 70. .213 of consensus"
5634. .15733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MIR repeat: matches 23. .147 of consensus" 0933. .31124
                                                                                                                                                                                                                       .175 of consensus"
                                       note="MER3 repeat: matches 4. .209 of consensus"
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8439. .28570
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note="8 copies 4 mer acac 87% conserved"
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                                                                                                                                                                                                                    note="MIR repeat: matches 81.
match: GSS: Em:AQ312069"
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DOE Joint Genome Institute.

Direct Submission

Submitted (03-402199) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases 1 to 159423)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (05-NOV-2002) DOB Joint Genome Institute, 2800 Mitchell
Brive, Walnut Creek, CA 9498, USA
On Nov 5, 2002 this sequence version replaced gi:15290285.
Draft Sequence Produced by DOB Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryoca, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC008429 159423 bp DNA linear PRI 05-NOV
Homo sapiens chromosome 5 clone CTC-308K20, complete sequence.
AC008429
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44070. .44541
/note="MER44B repeat: matches 1. .533 of consensus"
45723. .45777
/note="MADE1 repeat: matches 31. .80 of consensus"
45848. .45909
/note="MIR repeat: matches 148. .207 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                        Unclassified.

1 (bases 1 to 61)

Been, Wh.D., Rosenstein,S.P. and Perrotta,A.T.
Expwartic RNA molecules
Patent: US 5625047-A 18 29-APR-1997;

Location/Qualifiers
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llarity 58.5%; Pred. No. 8e+02;
Conservative 16; Mismatches
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Sequence 18 from patent US 5625047.
141390
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    .61
    /organism="unknown"

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                                                                                                                                                                                                                                                                                                                                                          GI:2081980
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nes 27; Conserv
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132535: contig of 35323 bp in length
132635: gap of 100 bp
171914: contig of 39279 bp in length.
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97212: gap of 100
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132636
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Dipublished

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Barten, V., Bloom, T., Boguslavky, L., Boukhgalter, B., Brom, A., Colangelo, M., Collins, S., Collymore, A., Chang, J., Cook, A., Cooke, P., DeAreallano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Fareiraia, P., FitzHugh, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Lander, A., Karatas, A., Karatas, A., Karatas, A., Karatas, A., Karatas, A., Kals, C., LaRoque, K., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C., MacCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Minova, T., Manga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Morbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Staltos, R., Schauer, S., Schupback, R., Stantos, S., Schupback, R., Stantos, J., Thedorer, J., Viel, R., Wola, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Kainer, S., Misson, B., Mu, X., Wyman, D., Ye, W.J., Young, G., Kainer, Submission
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                                                                                                                                                                                                                                                                                                                                                             /note="Shatter libraries failed to resolve dinucleotide repeat region from 21938 to 21990. Forced join at 21980."
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Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 171914)
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                     www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Bstimated Total Number of Errors is 0.1.
NOTE: Shatter libraries failed to resolve dinucleotide repeat
region from 21938 to 21990. Forced join at 21980.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.3%; Score 29.8; DB 9; Length 159423; Best Local Similarity 49.1%; Pred. No. 6.46+02; Matches 26; Conservative 13; Mismatches 14; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 CCACCUCCUCGCGGUNNNDNNUGGCCAUGCGGCUUCGCAUGGCUAAGGGACCC
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-321G8
                                                                                                                                                                            1. .159423
/organiam="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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HTG; HTGS PHASEL; HTGS DRAFT.
MUS mUSCULUS (house mouse)
MUS mUSCULUS
                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                          /clone="CTC-308K20"
21938. .21990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
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AC119266
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Diaz, J.S., Dodge, S., Dooley, K., Dotrie, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pletare, M., Hafez, M., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalis, C., Landers, T., Levine, R., Lindblad, Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Malora, T., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Maneus, L., Mhova, T., O'Donnell, P., O'Neil, D. Oilver, J., Peterson, K., Phunkhang, P., Flerre, N., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Stener, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Taalams, J., Teffaye, S., Theodore, J., Topham, K., Travers, M., Vasiliev, H., Venkataraman, V., Zembek, L., Zimmer, A. and Zody, M. Dirett, S., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Dirett, S., Shitz, M., Milson, B., Mu, X., Milson, B., Mar, M., Milson, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17.4MR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 17, 2003 this sequence version replaced gi:259563367. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 169262 bases at least Q40
Consensus quality: 170279 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 176000; agarose-fp
Quality coverage: 10.1 in Q20 bases; sum-of-contigs
Quality coverage: 10.1 in Q20 bases; sum-of-contigs
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13872: gap of 100 bp

14646: contig of 674 bp in length

14746: gap of 100 bp

16119: contig of 1373 bp in length

16219: gap of 100 bp

17367: contig of 1148 bp in length

17467: gap of 100 bp

19014: contig of 1547 bp in length
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of 12335 bp in length
100 bp
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gap of 100 bp
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Mus musculus clone RP23-187D8, WORKING DRAFT SEQUENCE, 11 unordered
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 45.3%; Score 29.8; DB 2; Length 171914; Similarity 45.3%; Pred. No. 6.3e+02; 4; Conservative, 15; Mismatches 14; Indels 0;
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                                                                                                                         /clone lib="RPCI-24 Male Mouse BAC" 1. 13872 inote="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-187D8
                                                                                                                                                                                                                                                                                                                                                                                                                  19115. .31449
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'note="aggembly_fragment"
                                                                                                                                                                                                                                                             note="assembly_fragment"
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7468. .19014
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6220. .17367
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32636. 171914
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                                             organism="Mus musculus"
                                                               /mol_type="genomic DNA"
/db xref="taxon:10090"
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HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
location/Qualifiers
                                                                                                         clone="RP24-321G8"
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                                                                                                                                                                                                               vector side:left"
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                                                                                                                                                                                                  clone end:SP6
                                                                                                                                                                                                                                                                                         4747. .16119
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AUTHORS
TITLE
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FEATURES
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ORIGIN

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Direct Submission

Direct Submission

Bubmitted (10-APR-2022) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

CE 3 (bases 1 to 184032)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Gollymore, A., Cook, A., Cook, B., Carm, B., Derarellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Frereira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand, Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kals, G., Landers, T., Levine, R., Indels, C., Landers, T., Levine, R., Machan, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Maddrim, J., Meneus, L., Minow, T., Mahditt, R., Machean, C., Maconald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Mandrim, J., Meneus, L., Minow, T., Mahditt, R., Machen, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., S., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev'H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Vassiliev'H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Vassiliev'H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Mu, X., Vielle, C., Shangeler, M. Research, 320 Charles Street, Cambridge, MA 02141, USA
Research, 320 Charles Green, P. (1996-1997)
Rhttp://ftp:genome.washington.edu/RW/RepeatMasker.html
Research, 2120 Charles Charle
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Nell,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Rettel,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Seaman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Strauss,N., Subramandan,A., Taylera, Tropham, Travis,N., Taylera, Trigillo,J., Vassillev,H., Viel,R., Vo,A., Wilson,B., Wi,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently a consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 182000; agarose-fp
Insert size: 183032; sum-of-contigs
Quality coverage: 10.8 in Q20 bases; agarose-fp
Quality coverage: 10.7 in Q20 bases; sum-of-contigs
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Web site: http://www-seq.wi.mit.edu
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Query Match 52.3%; Score 29.8; DB 2; Length 184032; Best Local Similarity 45.3%; Pred. No. 6.38+02; Matches 24; Conservative 15; Mismatches 14; Indels 0;
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Search completed: May 19, 2004, 03:57:14 Job time : 3052 secs

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May 19, 2004, 02:59:41; Search time 390 Seconds (without alignments) 663.253 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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	Description	Seguence 40, Appl	Sequence 80, Appl	Sequence 40, Appl	Sequence 80, Appl	Sequence 12, Appl	Sequence 13, Appl	Sequence 2, Appli	Sequence 7, Appli	Sequence 8, Appli	Sequence 4, Appli	Sequence 1, Appli	Sequence 2716, Ap	Sequence 10300, A	Sequence 6, Appli
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	Score	29.6	29.6	29.6	29.6	29.6	29.6	29.6	29.6	29.6	29.6	29.6	29.5	29.5	29.5
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1415 13 US-10-342-887-515 1415 13 US-10-172-118-515 1445 14 US-10-109-860-1 9704 14 US-10-109-860-3	15 1 15 1		13 16 16 17 18 18	15 113 115 12 13 13
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## ALIGNMENTS

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Sequence 40, Application US/10150407

Publication No. US20040029278A1

GENERAL INFORMATION:

APPLICANT: Dubensky Jr, Thomas W

Jolly, Douglas J.

TITLE OF INVENTION: BUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS

NUMBER OF SEQUENCES: 128

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: $300 Columbia Center, 701 Fifth Avenue

STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/150,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/350,522 FILING DATE: 08-Jul-1999 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17-May-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
RESULT 1
US-10-150-407-40
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GENERAL INFORMATION:
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ORGANISM: Unknown
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                   US-10-346-880-40
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Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DOOR SHOWN W. POLICANT: DOOR OF THE POLO, John M. Dollo, John M. Dollow, Douglas J. Driver, David A. TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYER: RIOPRY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRIT APPLICATION DATE: 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MCMAGEER, David D.
REGISTRATION NUMBER: 33,963
REFERENCE DOCKET NUMBER: 930049.423D1 / 1146.010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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12; Mismatches
                                                                                                                                                                     51.9%; Score 29.6; D
59.4%; Pred. No. 21;
tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/350,522
FILING DATE: 08-Jul-1999
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.9%; Score 29.6; 59.4%; Pred. No. 21
                                                                                                       ; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-150-407-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 80:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 80, Application US/10150407
Publication No. US20040029278A1
GENERAL INFORMATION:
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                 SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
INFORMATION FOR SEQ ID NO: 40:
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Best Local Similarity 59.44
Matches 19; Conservative
                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                               Conservative
                                                                                                                                                                   Query Match
Best Local Similarity
Matches 19; Conserva
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PatentIn version 3.0
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                                                                                                                                                                Best Local Similarity
Matches 19; Conserv
                                                               ; TYPE: DNA
; ORGANISM: HDV-REV
US-09-733-042-13
                         SEQ ID NO 13
LENGTH: 90
                                                                                                                                                 Query Match
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        SOFTWARE:
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APPLICANT: Hennecke, Frank
TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
FILE REFERENCE: 1700.0100001
CURRENT APPLICATION NUMBER: US/09/733,042
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 60/169,988
PRIOR PLILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
TVOS
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APPLICANT: Renner, Wolfgang A.
TITLE OF INVENTION: Replicon Based Activation of Endogenous Genes
FILE REPERBUCE: 1700.010001
CURRENT APPLICATION NUMBER: US/09/733,042
CURRENT PILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 60/169,988
PRIOR PELING DATE: 1999-12-10
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59.4%; Pred. No. 21;
tive 12; Mismatches
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59.4%; Pred. No. 23;
ive 12; Mismatches
PRIOR APPLICATION NUMBER: 08/404,796
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: 08/376,184
PRIOR PILING DATE: 1995-01-18
PRIOR PILING DATE: 1994-01-18
PRIOR PILING DATE: 1994-11-30
PRIOR PILING DATE: 1994-11-30
PRIOR PILING DATE: 1994-02-18
PRIOR FILING DATE: 1994-02-18
PRIOR FILING DATE: 1993-09-15
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PRACESEQ FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/09733042
Patent No. US20020168709A1
GENERAL INFORMATION:
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Best Local Similarity 59.4%
Matches 19, Conservative
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Best Local Similarity 59.44
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Unknown
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; ORGANISM: HDV-FOR
US-09-733-042-12
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                                                         Gaps
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APPLICANT: Li, Xiaomao
APPLICANT: Li, Xiaomao
APPLICANT: Klein, Michel
TITLE OP INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
FILE REPERENCE: Parrington et al.
CURRENT APPLICATION NUMBER: US/09/190,246
CURRENT FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 90
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  DB 9; Length 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Alphavax, Inc.
APPLICANT: Alphavax, Inc.
APPLICANT: Gonathan F. Smith
APPLICANT: Kurt I. Kamrud
APPLICANT: Kurt I. Kamrud
APPLICANT: Sergey A. Dryga
APPLICANT: Sergey A. Dryga
APPLICANT: Ian J. Caley
TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS
FILE REFERENCE: 01113.0002U2
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 60/317,722
PRIOR APPLICATION NUMBER: 60/317,722
PRIOR APPLICATION NUMBER: 60/317,722
PRIOR APPLICATION NUMBER: 60/317,722
PRIOR SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                       4 UCCACCUCCUCGCGGUNNNDNNUGGGCAUGCG 35
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59.4%; Pred. No. 23;
tive 12; Mismatches
51.9%; Score 29.6; I
59.4%; Pred. No. 23;
iive 12; Mismatches
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, Sequence 2, Application US/09190246
; Publication No. US20030180257A1
; GENERAL INFORMATION:
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Publication No. US20030119182A1
GENERAL INFORMATION:
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; ORGANISM: Semliki Forest virus
US-09-190-246-2
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ORGANISM: Artificial Sequence
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Sequence 1, Application US/09190246 Publication No. US20030180257A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Semliki Forest virus
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ORGANISM: Homo sapiens
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Matches 19; Conserve
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Matches 23; Conserva
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US-09-918-995-10300/c
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US-09-918-995-2716/c
                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 15538
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                                                        US-09-190-246-1
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                                        Gaps
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APPLICANT: L1, Xtaomao
APPLICANT: L1, Xtaomao
APPLICANT: K. Ataomao
APPLICANT: K. Ataomao
APPLICANT: K. Ataomao
TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
FILE REPREBRENCE: Parrington et al.
CURRENT APPLICATION VMBRR: US/09/190,246
CURRENT APPLICATION VMBRR: 1998-11-13
SOFTWARR: Patentin Ver: 2.0
SEQ ID NO 4
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   Length 91;
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                                     Indels
                                                                                                                                                                                                US-120-24-26/C

US-24-24-26/C

Sequence 8, Application US/1023302

Publication No. US20030119182A1

GENERAL INFORMATION:

APPLICANT: AlphaVax. Inc.

APPLICANT: Jonathan F. Smith

APPLICANT: Jonathan O. Rayner

APPLICANT: Jonathan O. Rayner

APPLICANT: Jonathan O. Rayner

APPLICANT: Ban J. Caley

TITLE OF INVENTION: ALPHAVIRUS REPLICON VECTOR SYSTEMS

FILE REFERENCE: 01113.000202

CURRENT APPLICATION NUMBER: US/10/237,302

CURRENT APPLICATION NUMBER: 60/317,722

PRIOR APPLICATION NUMBER: 60/317,722

PRIOR FILING DATE: 2001-09-06

NUMBER OF SEQ ID NOS: 49

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: DATE OF SEQ ID WINDOWS VERSION A.0

SEQ ID NO 8
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Pred. No. 37;
   DB 15;
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59.4%; Pred. No. 23;
tive 12; Mismatches
ch 51.9%; Score 29.6; D
1 Similarity 59.4%; Pred. No. 23; 19; Conservative 12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Semliki Forest virus
US-09-190-246-4
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Best Local Similarity 59.44
Matches 19; Conservative
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hes 19; Conservative
                     Best Local Similarity
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   Query Match
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Matches
                                        Matches
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APPLICANT: Parrington, Mark
APPLICANT: Li, Xiaomao
APPLICANT: Li, Xiaomao
APPLICANT: Li, Xiaomao
TTILE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
FILE REPERENCE: Parrington et al.
CURRENT APPLICATION NUMBER: US/09/190,246
CURRENT PILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 2.0
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2216
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; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            51.9%; Score 29.6; I
59.4%; Pred. No. 40;
tive 12; Mismatches
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Gaps

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DB 13; Length 1415;

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1 GGGUCCACCUCCUCGCGGUNNNDNNUGGGCAUGCGGCUUCGCAUGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.2%; Score 29.2; I 50.0%; Pred. No. 42; tive 13; Mismatches
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR PLING DATE: 2002-05-14
PRIOR PLING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR APPLICATION NUMBER: 10/172,118
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: May 19, 2004, 04:59:42 Job time : 421 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 50.04 Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-10-342-887-515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Publication No. US20020142421A1
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: ISOLATED HUMAN AMINOACYLASE, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN AMINOACYLASE, AND USES THEREOF
FILE REPERENCE: CLO01179DIV
CURRENT APPLICATION NUMBER: US/10/109,860
CURRENT FILING DATE: 2002-04-01
PRIOR FILING DATE: 2001-03|23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Non't Veer, Lianta Johanna
APPLICANT: Van 't Veer, Lianta Johanna
APPLICANT: Van 'd Veer, Lianta Johanna
APPLICANT: Van 'd Veer, Lianta Johanna
APPLICANT: Van de Vijevr, Marc J.
APPLICANT: Van 'd Veer, Lianta Johanna
APPLICANT: Van 'd Veer, Lian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 GGGTGCTCCTCCTCGGGACCCTTGCTGGTCATGGCGCTGCGCGTGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGGUCCACCUCCUCGCGGUNNNDNNUGGGCAUGCGGCUUCGCAUGG 46
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50.0%; Pred. No. 38;
tive 13; Mismatches
       FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: -US/09/918,995
CURRENT FILING DATE: 2001-70-30
FRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10300
LENGTH: 487
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                                                                                                                                                                                                                                                                                                                                                                                                                 | FEATURE:
| NAME/KEY: misc feature
| LOCATION: (1)...(487)
| CTHER INFORMATION: n = A,T,C or G
| US-09-918-995-10300
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Best Local Similarity 50.0%
Matches 23, Conservative
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Best Local Similarity 50.00
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-342-887-515/c
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LENGTH: 601
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